

IN THE CLAIMS

Please amend the claims as follows:

Claim 1 (Original): Isolated nucleic acid sequence coding for a polypeptide having acetohydroxy acid synthetase (AHAS) activity selected from the group consisting of:

- a) a nucleic acid sequence according to SEQ. ID No: 1 or SEQ. ID NO: 3;
- b) a nucleic acid sequence comprising in position 21 and 22 a base triplet coding for Asp and Phe, respectively;
- c) a nucleic acid sequence hybridising under stringent conditions with those of a) or b);
- d) a nucleic acid sequence having a homology of at least 70% with those of a) or b);
- e) a nucleic acid coding for a polypeptide having at least 80% homology on amino acid level with the polypeptide coded by a) or b);
- f) a nucleic acid coding for a polypeptide with improved activity and/or selectivity and/or stability as compared with the polypeptide coded by a) or b), prepared by
 - i) mutagenesis of a nucleic acid of a) or b),
 - ii) ligating the nucleic acid sequence obtainable from i) into a suitable vector followed by transformation into a suitable expression system and
 - iii) expression and detection of the critical polypeptide with improved activity and/or selectivity and/or stability;
- g) polynucleotide containing at least 15 successive bases of the polynucleotide sequences of a) - f).

Claim 2 (Original): A polypeptide selected from the group consisting of:

- a) a polypeptide coded by a nucleic acid sequence according to Claim 1;
- b) a polypeptide having a sequence in accordance with SEQ. ID NO: 2 or SEQ. ID NO: 4;
- c) a polypeptide which is at least 84% homologous to a polypeptide with SEQ. ID NO: 2 or SEQ: ID NO. 4, without the activity and/or selectivity and/or stability of the polypeptide being substantially reduced as compared with the polypeptide with SEQ. ID NO: 2 or SEQ. ID NO: 4.

Claim 3 (Currently Amended): Plasmids, vectors, micro-organisms comprising one or more nucleic acid sequences according to ~~Claims~~ Claim 1.

Claim 4 (Original): Primers for preparing - by means of PCR - or hybridisation probes for detecting the nucleic acid sequences according to Claim 1.

Claim 5 (Original): A process for preparing improved rec-polypeptides with acetohydroxy acid synthetase (AHAS) activity starting from nucleic acid sequences in accordance with Claim 1,

characterised in that

- a) the nucleic acid sequences are subjected to mutagenesis,
- b) the nucleic acid sequences obtainable from a) are cloned in a suitable vector and these are transferred into a suitable expression system and
- c) the polypeptides with improved activity and/or selectivity and/or stability which are formed are detected and isolated.

Claim 6 (Original): rec-polypeptides or nucleic acid sequences coding for these, obtainable in accordance with Claim 5.

Claim 7 (Currently Amended): The use of the polypeptides in accordance with Claim 2 or 6 to prepare enantiomer-enriched branched-chain amino acids.

Claim 8 (Currently Amended): Use of the nucleic acid sequences in accordance with Claim 1 or 6 to prepare an amino acid producing micro-organism.

Claim 9 (Original): Process for the production of a branched-chain amino acid using a polypeptide of Claim 2.

Claim 10 (Original): Vector pECKA or pECKA/ilvBNC.

Claim 11 (Original): Micro-organisms: DSM15652, DSM15651, DSM15650.